```
      10        20        30        40        50        60        70        80        90
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890
ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA AATGAATGGC ACTTATGACT ACAGTCAATA TGAACTGATC   90
M  A  L  E  Q  N  Q  S  T  D  Y  Y  Y  E  E  N  E  M  N  G  T  Y  D  Y  S  Q  Y  E  L  I

TGTATCAAAG AAGATGTCAG AGAATTTGCA AAAGTTTTCC TCCCTGTATT CCTCACAATA GTTTTCGTCA TTGGACTTGC AGGCAATTCC  180
C  I  K  E  D  V  R  E  F  A  K  V  F  L  P  V  F  L  T  I  V  F  V  I  G  L  A  G  N  S

ATGGTAGTGG CAATTTATGC CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC CTGAATTTGG CTGTAGCAGA TTTACTCCTT  270
M  V  V  A  I  Y  A  Y  Y  K  K  Q  R  T  K  T  D  V  Y  I  L  N  L  A  V  A  D  L  L  L

CTATTCACTC TGCCTTTTTG GCTGTTAAT GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC CTTGTACACA  360
L  F  T  L  P  F  W  A  V  N  A  V  H  G  W  V  L  G  K  I  M  C  K  I  T  S  A  L  Y  T

CTAAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGTATCA GCATAGACAG ATATGTGGCA GTAACTAAAG TCCCCAGCCA ATCAGGAGTG  450
L  N  F  V  S  G  M  Q  F  L  A  C  I  S  I  D  R  Y  V  A  V  T  K  V  P  S  Q  S  G  V

GGAAAACCAT GCTGGATCAT CTGTTTCTGT GTCTGGATGG CTGCCATCTT GCTGAGCATA CCCCAGCTGG TTTTTTATAC AGTAAATGAC  540
G  K  P  C  W  I  I  C  F  C  V  W  M  A  A  I  L  L  S  I  P  Q  L  V  F  Y  T  V  N  D

AATGCTAGGT GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT CAAATGCTAG AGATCTGCAT TGGATTTGTA  630
N  A  R  C  I  P  I  F  P  R  Y  L  G  T  S  M  K  A  L  I  Q  M  L  E  I  C  I  G  F  V

GTACCCTTTC TTATTATGGG GGTGTGCTAC TTTATCACAG CAAGGACACT CATGAAGATG CCAAACATTA AAATATCTCG ACCCCTAAAA  720
V  P  F  L  I  M  G  V  C  Y  F  I  T  A  R  T  L  M  K  M  P  N  I  K  I  S  R  P  L  K

GTTCTGCTCA CAGTCGTTAT AGTTTTCATT GTCACTCAAC TGCCTTAATA CATTGTCAAG TTCTGCCGAG CCATAGACAT CATCTACTCC  810
V  L  L  T  V  V  I  V  F  I  V  T  Q  L  P  Y  N  I  V  K  F  C  R  A  I  D  I  I  Y  S

CTGATCACCA GCTGCAACAT GAGCAAACGC ATGGACATCG CCATCCAAGT CACAGAAAGC ATCCCACTCT TTCACAGCTG CCTCAACCCA  900
L  I  T  S  C  N  M  S  K  R  M  D  I  A  I  Q  V  T  E  S  I  A  L  F  H  S  C  L  N  P

ATCCTTTATG TTTTTATGGG AGCATCTTTC AAAAACTACG TTATGAAAGT GGCCAAGAAA TATCGGTCCT GGAGAAGACA GAGACAAAGT  990
I  L  Y  V  F  M  G  A  S  F  K  N  Y  V  M  K  V  A  K  K  Y  G  S  W  R  R  Q  R  Q  S

GTGGAGGAGT TTCCTTTTGA TTCTGAGGGT CCTACAGAGC CAACCAGTAC TTTTAGCATT TAAAGGTAAA ACTGCTCTGC CTTTTGCTTG 1080
V  E  E  F  P  F  D  S  E  G  P  T  E  P  T  S  T  F  S  I  .  R  .  N  C  S  A  F  C  L

GATACATATG AATGATGCTT TCCCCTCAAA TAAAACATCT GCCTTATTCT GAAAAAAAAA AAAAAAM                      1147
D  T  Y  E  .  C  F  P  L  K  .  N  I  C  L  I  L  K  K  K  K  K
```

FIG. 1
(SEQ. ID NO: 1 & 2)

A

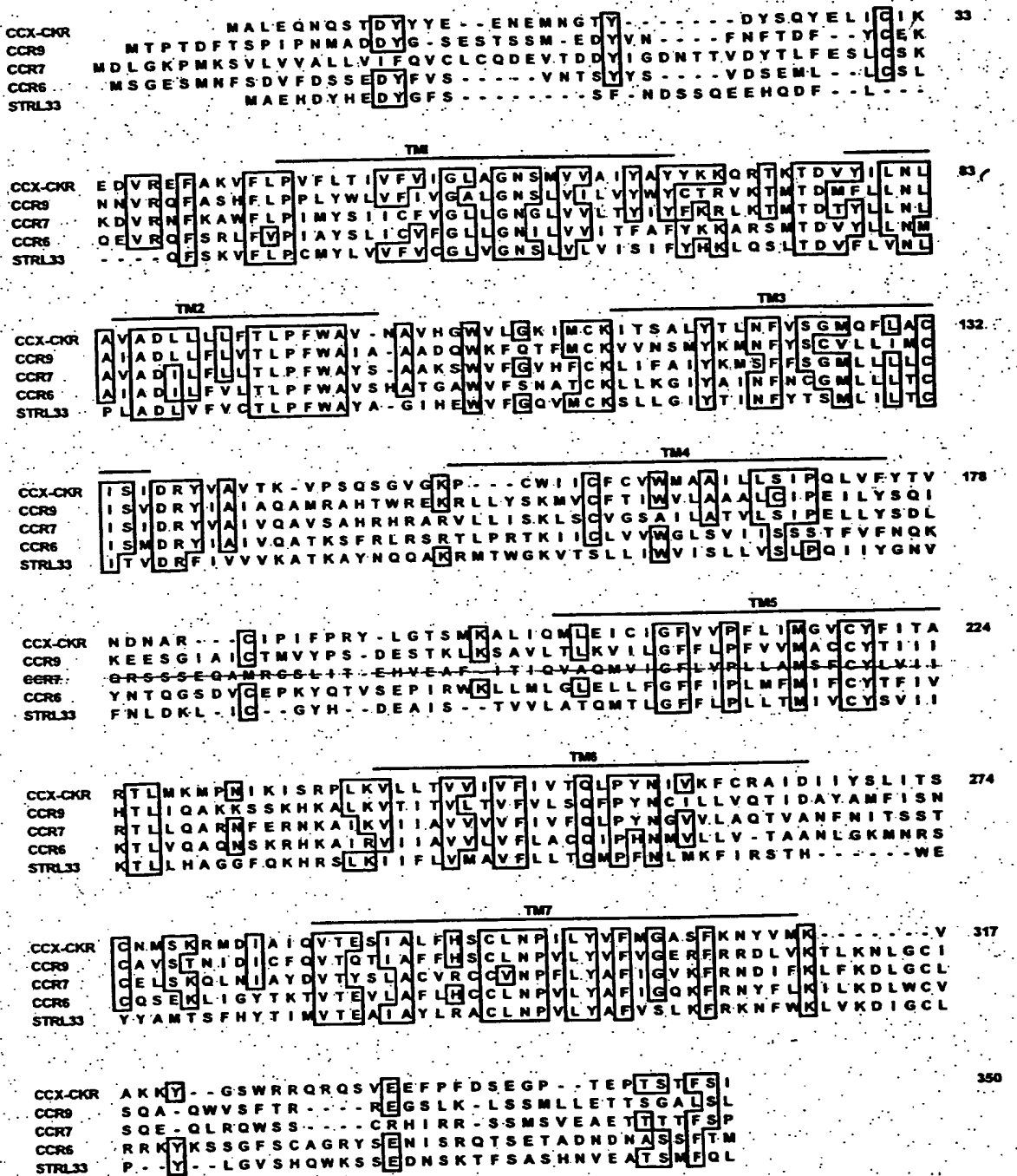


FIG. 2(a)

B

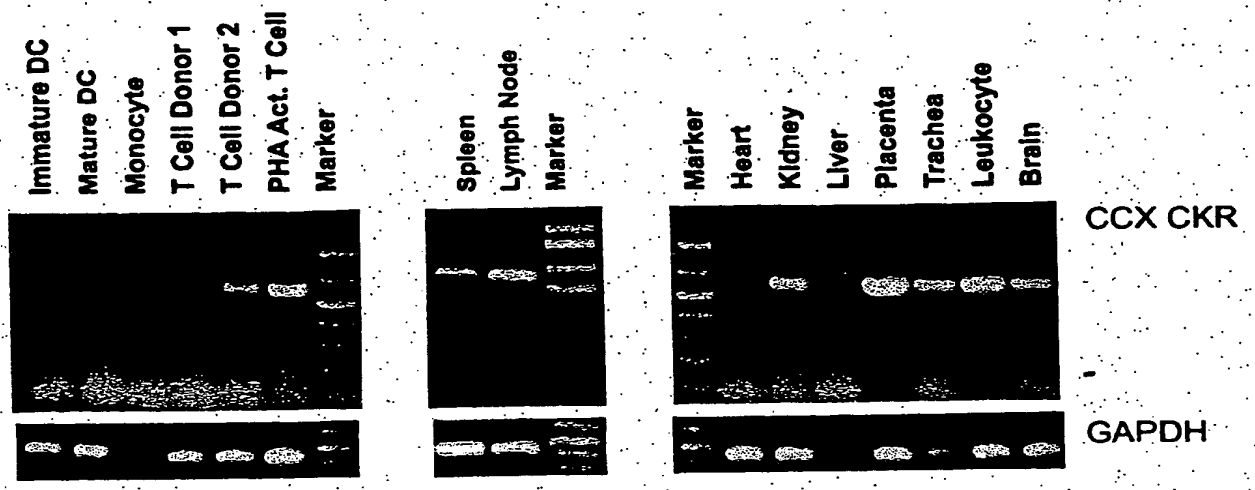


FIG. 2(b)

C

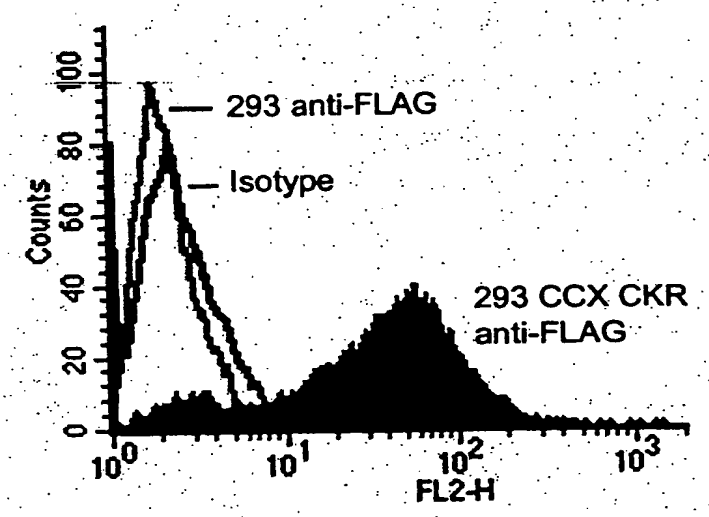
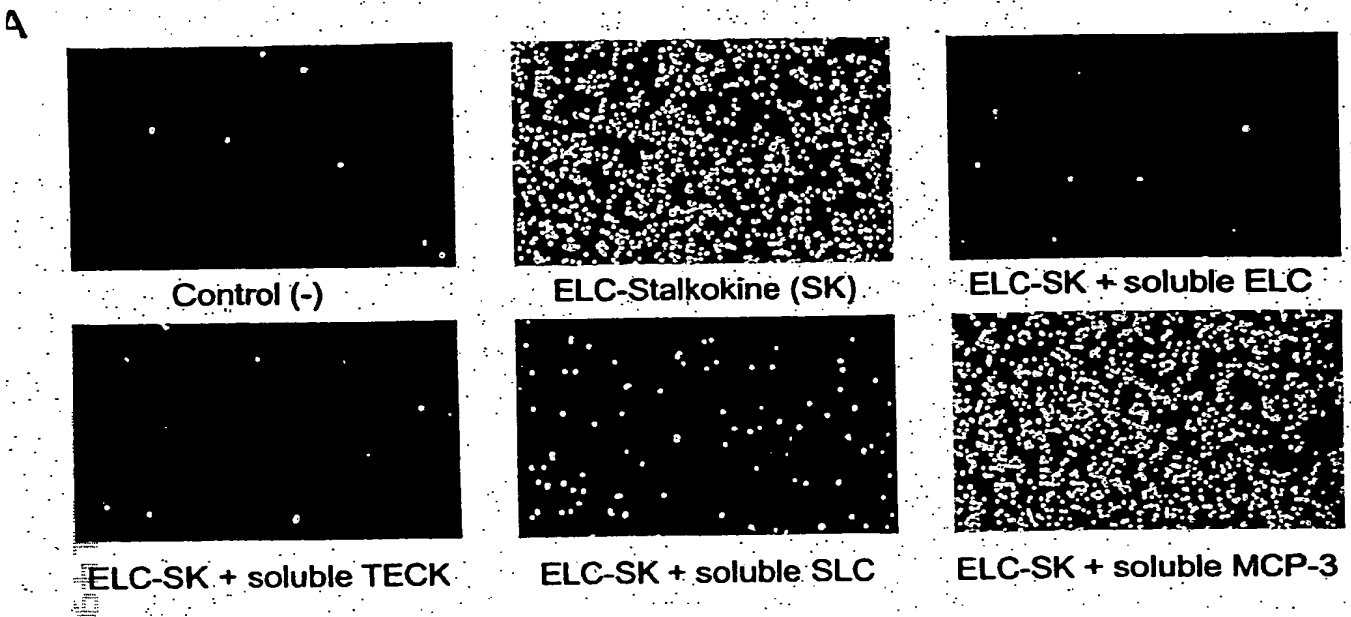


FIG. 2(c)

FIG. 3(a)



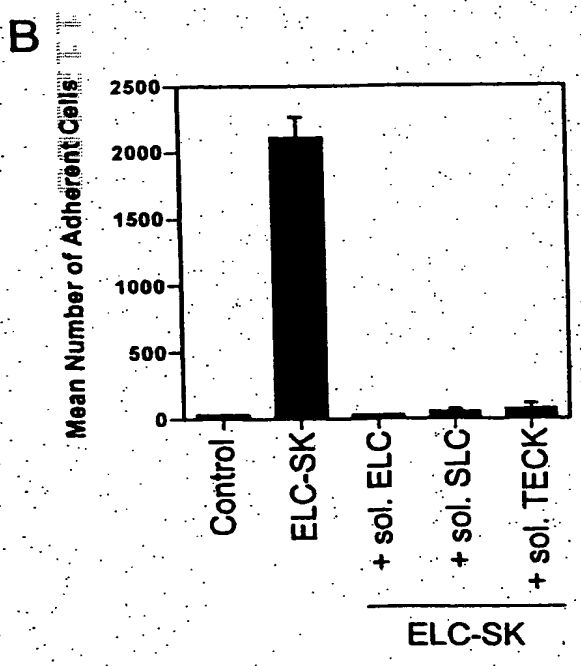


FIG. 3(b)

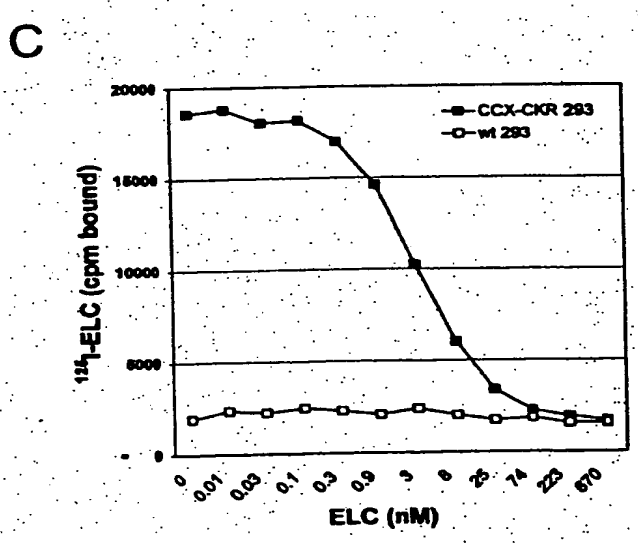


FIG. 3(c)

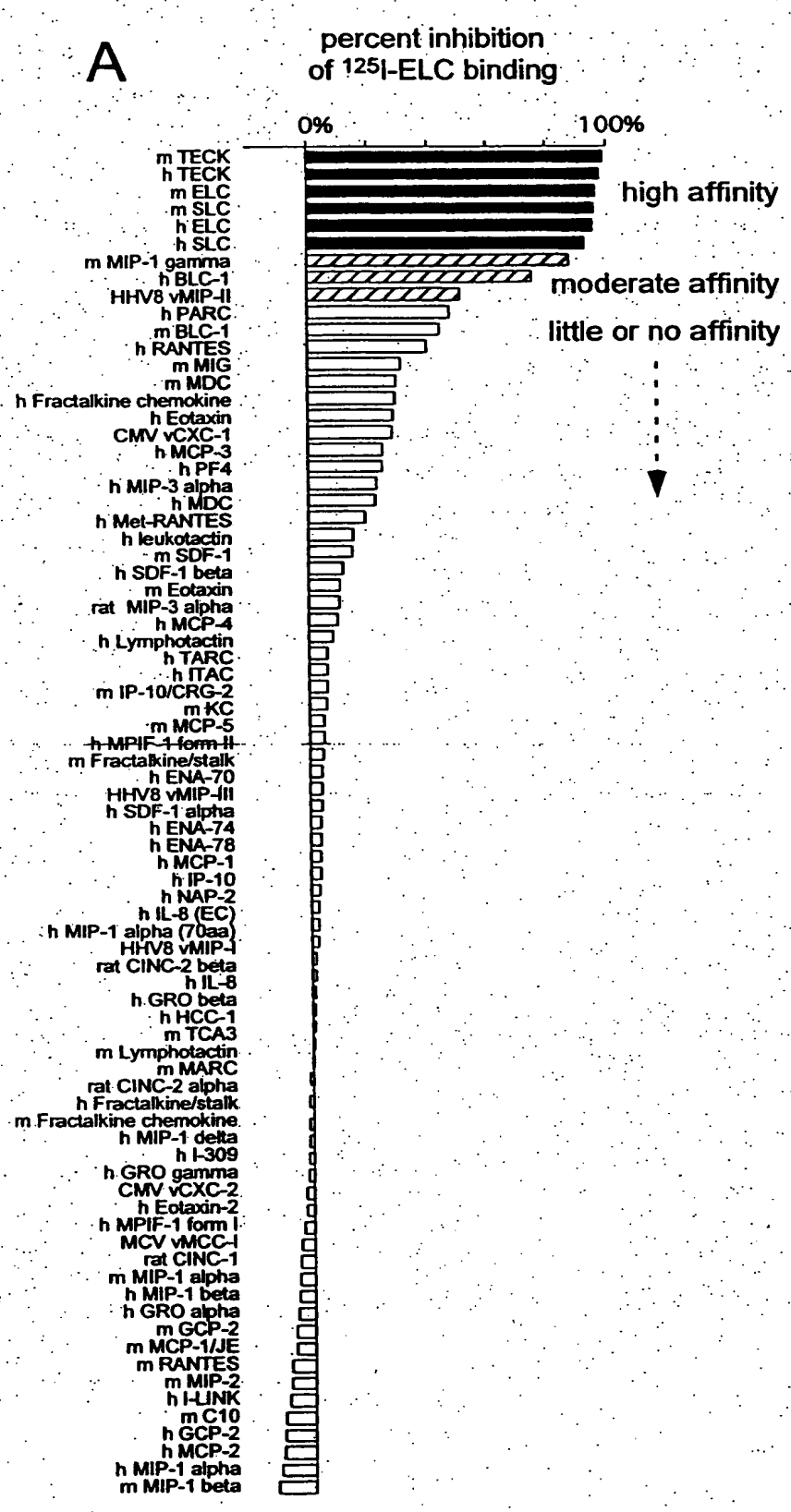
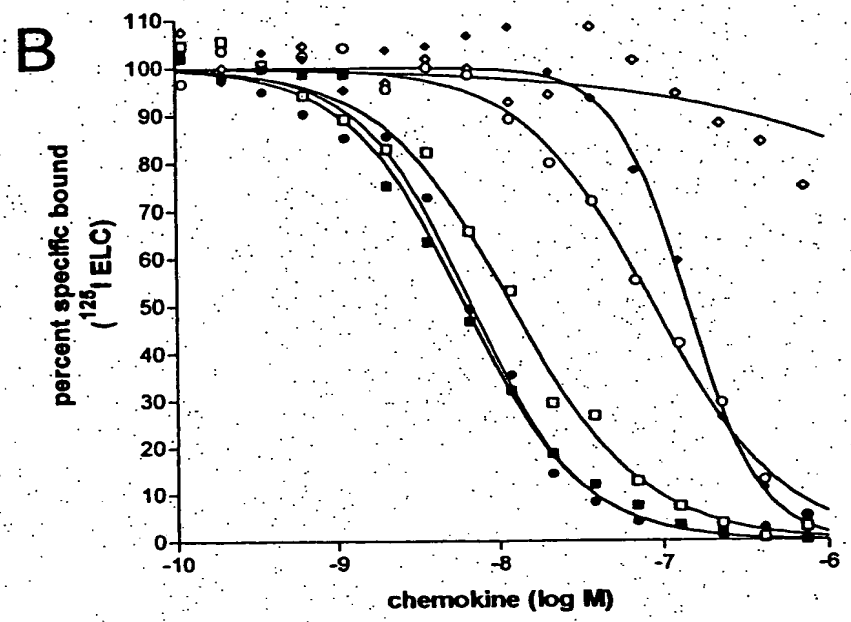

A
percent inhibition
of 125I-ELC binding
0%
100%
high affinity
moderate affinity
little or no affinity
m TECK
h TECK
m ELC
m SLC
h ELC
h SLC
m MIP-1 gamma
h BLC-1
HHV8 vMIP-II
h PARC
m BLC-1
h RANTES
m MIG
m MDC
h Fractalkine chemokine
h Eotaxin
CMV vCXC-1
h MCP-3
h PF4
h MIP-3 alpha
h MDC
h Met-RANTES
h leukotactin
m SDF-1
h SDF-1 beta
m Eotaxin
rat MIP-3 alpha
h MCP-4
h Lymphotactin
h TARC
h ITAC
m IP-10/CRG-2
m KC
m MCP-5
h MPIF-1 form II
m Fractalkine/stalk
h ENA-70
HHV8 vMIP-III
h SDF-1 alpha
h ENA-74
h ENA-78
h MCP-1
h IP-10
h NAP-2
h IL-8 (EC)
h MIP-1 alpha (70aa)
HHV8 vMIP-I
rat CINC-2 beta
h IL-8
h GRO beta
h HCC-1
m TCA3
m Lymphotactin
m MARC
rat CINC-2 alpha
h Fractalkine/stalk
m Fractalkine chemokine
h MIP-1 delta
h I-309
h GRO gamma
CMV vCXC-2
h Eotaxin-2
h MPIF-1 form I
MCV vMCC-I
rat CINC-1
m MIP-1 alpha
h MIP-1 beta
h GRO alpha
m GCP-2
m MCP-1/JE
m RANTES
m MIP-2
h I-LINK
m C10
h GCP-2
h MCP-2
h MIP-1 alpha
m MIP-1 beta

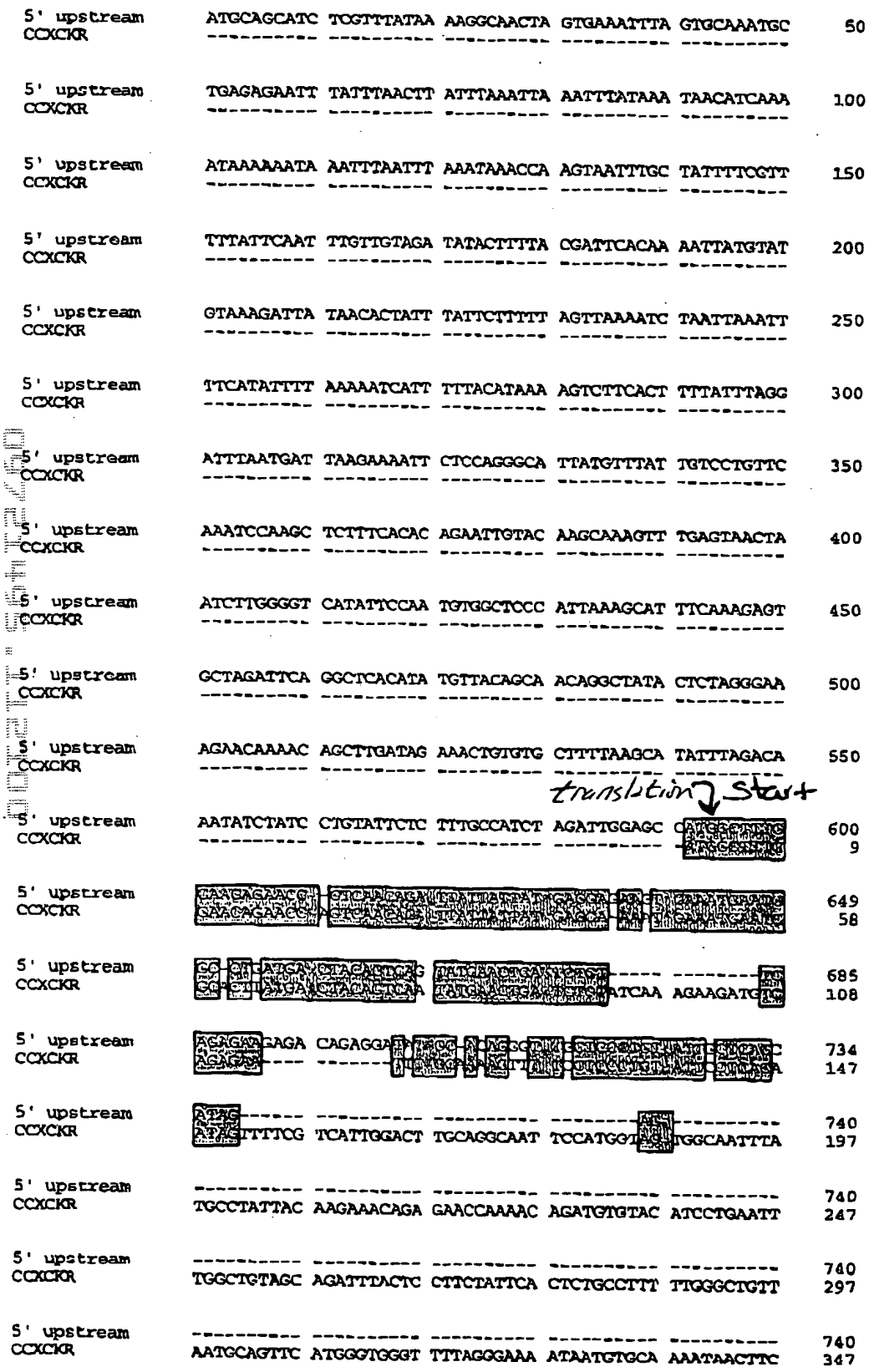
FIG. 4(a)



human chemokines	IC-50	murine chemokines	IC-50
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
● h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4(b)

FIG. 5


5' upstream
CCXCKR
ATGCAGCATC TCGTTTATAA AAGGCAACTA GTGAAAATTTA GTGCAAATGC 50
5' upstream
CCXCKR
TGAGAGAATT TATTTAACTT ATTTAAATTA AATTTATAAA TAACATCAAA 100
5' upstream
CCXCKR
ATAAAAAATA AATTTAATTT AAATAAACCA AGTAATTTGC TATTTTCGTT 150
5' upstream
CCXCKR
TTTATTCAAT TTGTTGTAGA TATACTTTTA CGATTCACAA AATTATGTAT 200
5' upstream
CCXCKR
GTAAAGATTA TAACACTATT TATTCTTTTT AGTTAAAATC TAATTAAATT 250
5' upstream
CCXCKR
TTCATATTTT AAAAATCATT TTTACATAAA AGTCTTCACT TTTATTTAGG 300
5' upstream
CCXCKR
ATTTAATGAT TAAGAAAATT CTCCAGGGCA TTATGTTTAT TGTCCTGTTC 350
5' upstream
CCXCKR
AAATCCAAGC TCTTTCACAC AGAATTGTAC AAGCAAAGTT TGAGTAACTA 400
5' upstream
CCXCKR
ATCTTGGGGT CATATTCCAA TGTGGCTCCC ATTAAAGCAT TTCAAAGAGT 450
5' upstream
CCXCKR
GCTAGATTCA GGCTCACATA TGTTACAGCA ACAGGCTATA CTCTAGGGAA 500
5' upstream
CCXCKR
AGAACAAAAC AGCTTGATAG AAACTGTGTG CTTTTAAGCA TATTTAGACA 550
translation start
5' upstream
CCXCKR
AATATCTATC CTGTATTCTC TTTGCCATCT AGATTGGAGC 600
9
5' upstream
CCXCKR
649
58
5' upstream
CCXCKR
685
108
5' upstream
CCXCKR
734
147
5' upstream
CCXCKR
740
197
5' upstream
CCXCKR
TGCCTATTAC AAGAAACAGA GAACCAAAAC AGATGTGTAC ATCCTGAATT 740
247
5' upstream
CCXCKR
TGGCTGTAGC AGATTTACTC CTTCTATTCA CTCTGCCTTT TTGGGCTGTT 740
297
5' upstream
CCXCKR
AATGCAGTTC ATGGGTGGGT TTTAGGGAAA ATAATGTGCA AAATAACTTC 740
347

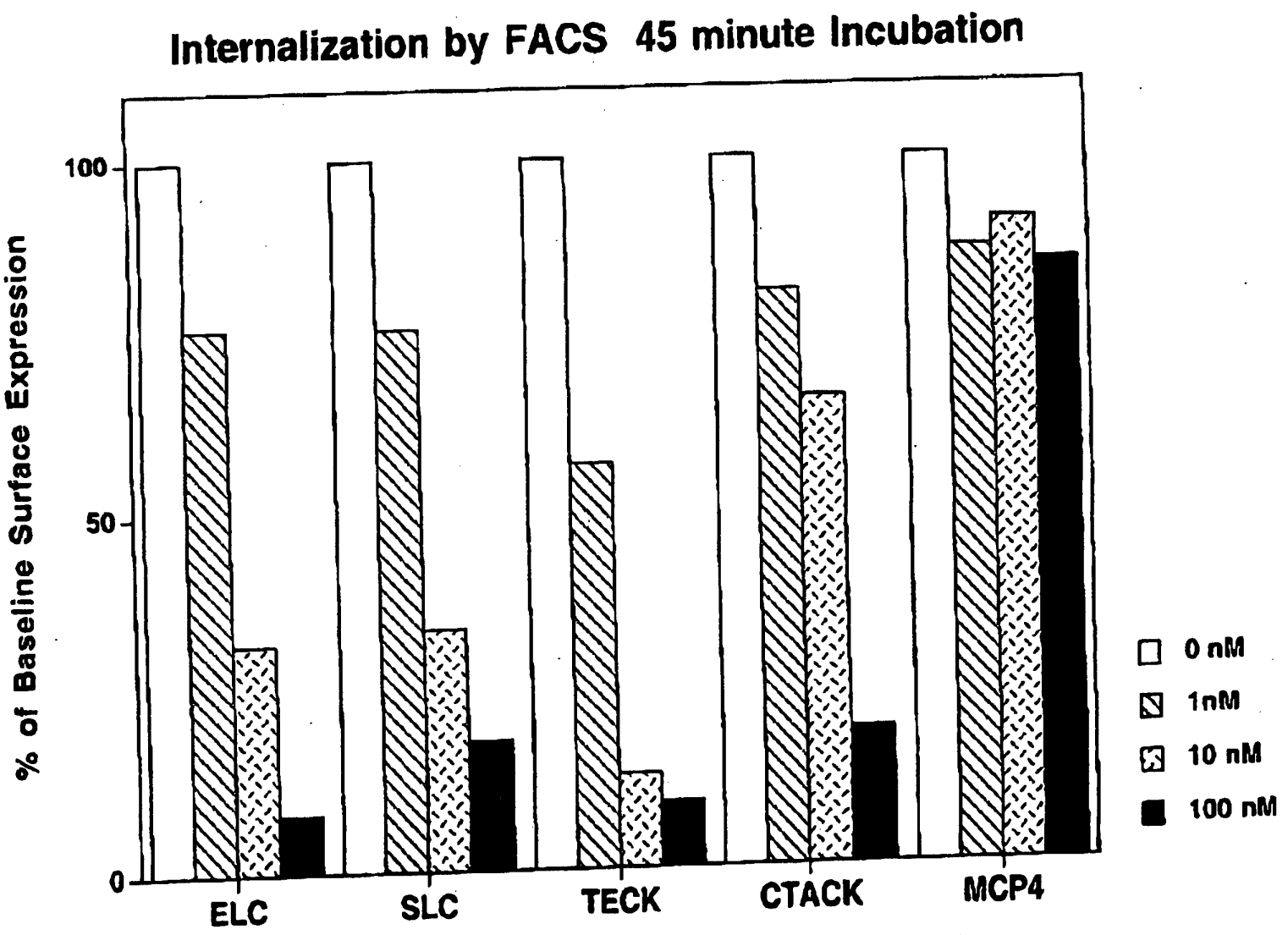


Fig. 6A

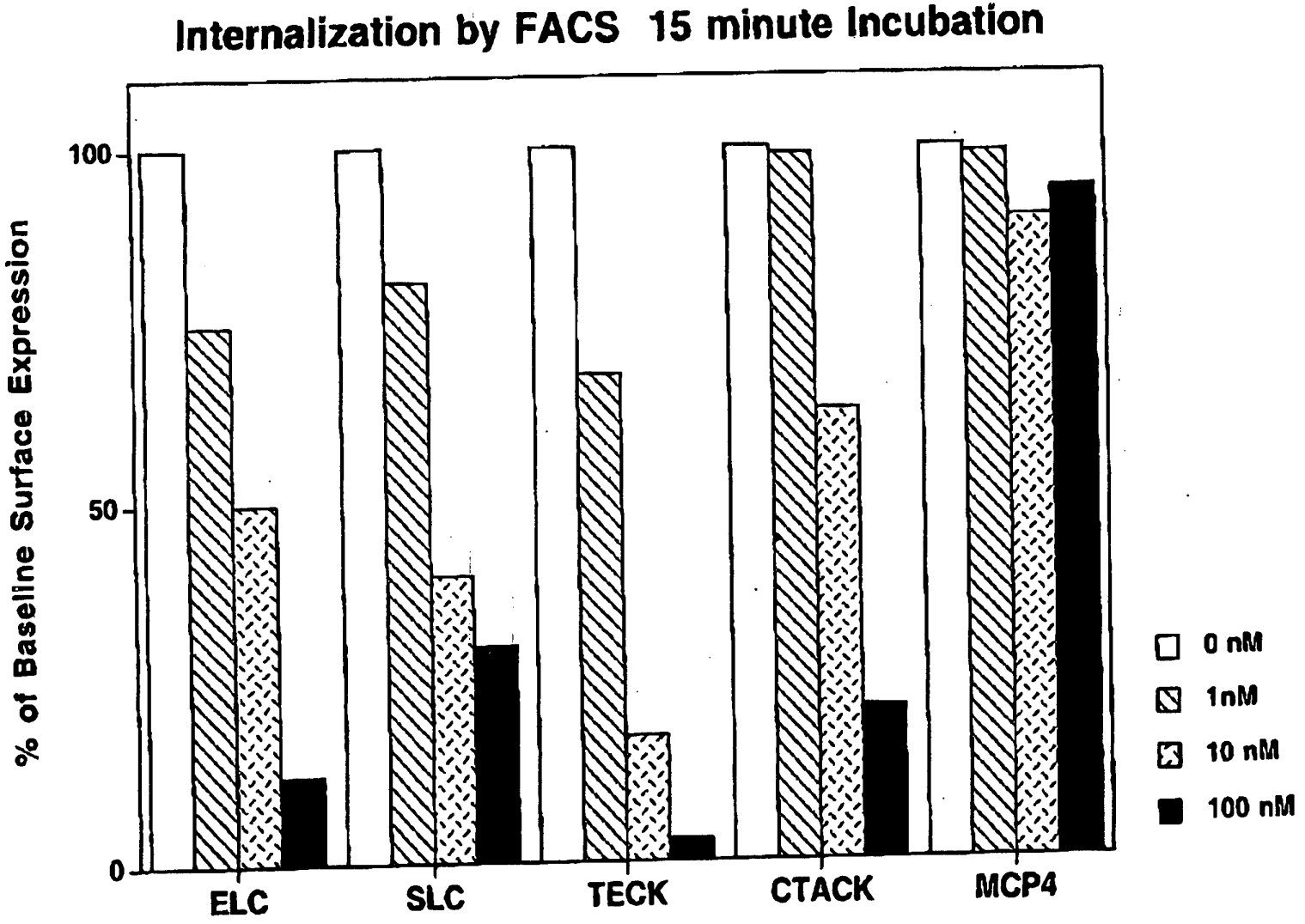


Fig. 6B